

## SEQUENCE LISTING



<110> Guss, Bengt  
 Nilsson, Martin  
 Frykberg, Lars  
 Flock, Jan-Ingmar  
 Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from  
 Coagulase-Negative Staphylococcus

*Sub C*  
 B  
 <130> guss 09/147405

<140> 09/147405  
 <141> 1999-04-01

<150> PCT/SE97/10191  
 <151> 1997-06-18

<150> SE 9602496-3  
 <151> 1996-06-20

<160> 15

<170> PatentIn Ver. 2.0

<210> 1  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 1  
 caacaaccat ctcacacaac

20

<210> 2  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 2  
 catcaaattg atatttccca tc

22

RECEIVED  
 TECH CENTER 1500/2000  
 99 OCT 26 PM:12:53

<210> 3  
<211> 18  
<212> DNA  
<213> *Staphylococcus epidermidis*

<400> 3  
gantcngant cnganagn

18

<210> 4  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 4  
aggtaaggaa caaggtgac

19

<210> 5  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 5  
ccgatgaaaa tggaaagtat c

21

<210> 6  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 6  
tccgttatct atactaaagt c

21

<210> 7

<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 7  
actgatcatg atgactttag t 21

<210> 8  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 8  
gcggatccaa tcagtcata aacaccgacg at 32

<210> 9  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 9  
cgaaattctg ttccggactga tttggaagtt cc 32

<210> 10  
<211> 1781  
<212> DNA  
<213> *Staphylococcus epidermidis*

<220>  
<221> CDS  
<222> (3)..(1781)

<400> 10  
ac cac cac cac cac cac ccc tct agt gat gaa gaa aag aat gat 47  
His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp  
1 5 10 15

gtg atc aat aat aat cag tca ata aac acc gac gat aat aac caa ata	95		
Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile			
20	25	30	
att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca	143		
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser			
35	40	45	
gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca	191		
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr			
50	55	60	
ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag	239		
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu			
65	70	75	
gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act	287		
Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr			
80	85	90	95
gcc caa caa cca tct cac aca aca ata aat aga gaa gaa tct gtt caa	335		
Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln			
100	105	110	
aca agt gat aat gta gaa gat tca cac gta tca gat ttt gct aac tct	383		
Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser			
115	120	125	
aaa ata aaa gag agt aac act gaa tct ggt aaa gaa gag aat act ata	431		
Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile			
130	135	140	
gag caa cct aat aaa gta aaa gaa gat tca aca aca agt cag ccg tct	479		
Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser			
145	150	155	
ggc tat aca aat ata gat gaa aaa att tca aat caa gat gag tta tta	527		
Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu			
160	165	170	175
aat tta cca ata aat gaa tat gaa aat aag gct aga cca tta tct aca	575		
Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr			
180	185	190	
aca tct gcc caa cca tcg att aaa cgt gta acc gta aat caa tta gcg	623		
Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala			
195	200	205	

gcg gaa caa ggt tcg aat gtt aac cat tta att aaa gtt act gat caa	671		
Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln			
210	215	220	
agt att act gaa gga tat gat gat agt gaa ggt gtt att aaa gca cat	719		
Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His			
225	230	235	
gat gct gaa aac tta atc tat gat gta act ttt gaa gta gat gat aag	767		
Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys			
240	245	250	255
gtg aaa tct ggt gat acg atg aca gtg gat ata gat aag aat aca gtt	815		
Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val			
260	265	270	
cca tca gat tta acc gat agc ttt aca ata cca aaa ata aaa gat aat	863		
Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn			
275	280	285	
tct gga gaa atc atc gct aca ggt act tat gat aac aaa aat aaa caa	911		
Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln			
290	295	300	
atc acc tat act ttt aca gat tat gta gat aag tat gaa aat att aaa	959		
Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys			
305	310	315	
gca cac ctt aaa tta acg tca tac att gat aaa tca aag gtt cca aat	1007		
Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn			
320	325	330	335
aat aat acc aag tta gat gta gaa tat aaa acg gcc ctt tca tca gta	1055		
Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val			
340	345	350	
aat aaa aca att acg gtt gaa tat caa aga cct aac gaa aat cgg act	1103		
Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr			
355	360	365	
gct aac ctt caa agt atg ttt aca aat ata gat acg aaa aat cat aca	1151		
Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr			
370	375	380	
gtt gag caa acg att tat att aac cct ctt cgt tat tca gcc aag gaa	1199		
Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu			
385	390	395	

aca aat gta aat att tca ggg aat ggt gat gaa ggt tca aca att ata	1247
Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile	
400 405 410 415	
gac gat agc aca ata att aaa gtt tat aag gtt gga gat aat caa aat	1295
Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn	
420 425 430	
tta cca gat agt aac aga att tat gat tac agt gaa tat gaa gat gtc	1343
Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val	
435 440 445	
aca aat gat gat tat gcc caa tta gga aat aat aat gat gtg aat att	1391
Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile	
450 455 460	
aat ttt ggt aat ata gat tca cca tat att att aaa gtt att agt aaa	1439
Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys	
465 470 475	
tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca	1487
Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr	
480 485 490 495	
atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc	1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser	
500 505 510	
tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt	1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly	
515 520 525	
gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa	1631
Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu	
530 535 540	
gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg	1679
Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro	
545 550 555	
ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa	1727
Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys	
560 565 570 575	
tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag	1775
Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln	
580 585 590	

gtc gac  
Val Asp

1781

<210> 11  
<211> 593  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 11  
His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp Val  
1 5 10 15  
  
Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile  
20 25 30  
  
Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu  
35 40 45  
  
Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe  
50 55 60  
  
Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val  
65 70 75 80  
  
Lys Glu Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala  
85 90 95  
  
Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr  
100 105 110  
  
Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys  
115 120 125  
  
Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Asn Thr Ile Glu  
130 135 140  
  
Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly  
145 150 155 160  
  
Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn  
165 170 175  
  
Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr  
180 185 190  
  
Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala

195 200 205  
Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser  
210 215 220  
Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp  
225 230 235 240  
Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val  
245 250 255  
Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro  
260 265 270  
Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser  
275 280 285  
Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile  
290 295 300  
Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala  
305 310 315 320  
His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn  
325 330 335  
Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn  
340 345 350  
Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala  
355 360 365  
Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val  
370 375 380  
Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr  
385 390 395 400  
Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp  
405 410 415  
Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu  
420 425 430  
Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr  
435 440 445  
Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile Asn

450 455 460  
Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr  
465 470 475 480  
Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr Met  
485 490 495  
Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr  
500 505 510  
Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp  
515 520 525  
Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp  
530 535 540  
Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu  
545 550 555 560  
Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser  
565 570 575  
Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln Val  
580 585 590  
Asp

<210> 12  
<211> 1744  
<212> DNA  
<213> *Staphylococcus epidermidis*  
  
<400> 12  
tctagtatg aagaaaagaa tgatgtgatc aataataatc agtcaataaa caccgacgat 60  
aataaccaa taattaaaaa agaagaaacg aataactacg atggcataga aaaacgctca 120  
gaagatagaa cagagtcaac aacaaatgta gatgaaaacg aagcaacatt tttacaaaag 180  
acccctcaag ataataactca tcttacagaa gaagaggtaa aagaatcctc atcagtcgaa 240  
tcctcaaatt catcaattga tactgcccaa caaccatctc acacaacaat aaatagagaa 300  
gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagattt tgctaactct 360

aaaataaaag agagtaaacac tgaatctggt aaagaagaga atactataga gcaaccta 420  
aaagtaaaag aagattcaac aacaagtcag ccgtctggct atacaatata agataaaaa 480  
atttcaaatac aagatgagtt attaaattta ccaataatg aatatgaaaa taaggctaga 540  
ccattatcta caacatctgc ccaaccatcg attaaacgtg taaccgtaaa tcaattagcg 600  
gcggaacaag gttcaatgt taaccatTTTA attaaagtta ctgatcaaag tattactgaa 660  
ggatatgatg atagtgaagg tgTTTttaaa gcacatgatg ctgaaaactt aatctatgat 720  
gtAACTTTG aagtagatga taaggtgaaa tctggtgata cgatgacagt ggatatagat 780  
aagaatacag ttccatcaga tttaaccgat agctttacaa taccaaaaaat aaaagataat 840  
tctggagaaa tcatcgctac aggtacttat gataacaaaa ataaacaaat cacctatact 900  
tttacagatt atgtagataa gtatgaaaat attaaagcac accttaaatt aacgtcatac 960  
attgataaat caaaggTTCC aaataataat accaagttag atgtagaata taaaacggcc 1020  
ctttcatcag taaataaaac aattacggtt gaatatcaaa gacctaacga aaatcggact 1080  
gctaaccTTc aaagtatgtt tacaatata gatacggaaa atcatacagt tgagcaaacg 1140  
atttatatta accctctcg ttattcagcc aaggaaacaa atgtaaatata ttcaGGGAat 1200  
ggtgatgaag gttcaacaat tatagacgt agcacaataa ttAAAGTTA taaggTTGGA 1260  
gataatcaaatttaccaga tagtaacaga atttatgatt acagtgaata tgaagatgtc 1320  
acaaatgatg attatGCCA atttagaaat aataatgatg tgaatattaa ttTTGGTAat 1380  
atagattcac catatattat taaagttatt agtaaatatg accctaataa ggatgattac 1440  
acgactatac agcaaactgt gacaatgcag acgactataa atgagtatac tggtagttt 1500  
agaacagcat cctatgataa tacaattgct ttctctacaa gttcaggtca aggacaagg 1560  
gacttgcctc ctgaaaaaac ttataaaatc ggagattacg tatggaaaga tgtagataaa 1620  
gatggtattc aaaatacAAA tgataatgaa aaaccgctt gtaatgtatt ggtAACTTTG 1680  
acgtatcctg atggaacttc aaaatcagtc agaacagatg aagatggaa atatcaattt 1740  
gatg

1744

<210> 13

<211> 581

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 13

Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn Gln Ser Ile  
1 5 10 15

Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn  
20 25 30

Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr  
35 40 45

Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp  
50 55 60

Asn Thr His Leu Thr Glu Glu Val Lys Glu Ser Ser Ser Val Glu  
65 70 75 80

Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser His Thr Thr  
85 90 95

Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val Glu Asp Ser  
100 105 110

His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu  
115 120 125

Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Lys Glu  
130 135 140

Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys  
145 150 155 160

Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu  
165 170 175

Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys  
180 185 190

Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val Asn  
195 200 205

His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp  
210 215 220

Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr Asp  
225 230 235 240

Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met Thr  
245 250 255

Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser Phe  
260 265 270

Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly  
275 280 285

Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr  
290 295 300

Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser Tyr  
305 310 315 320

Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val Glu  
325 330 335

Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu Tyr  
340 345 350

Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe Thr  
355 360 365

Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile Asn  
370 375 380

Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly Asn  
385 390 395 400

Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys Val  
405 410 415

Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr  
420 425 430

Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu  
435 440 445

Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro  
450 455 460

Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr  
465 470 475 480

Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu Tyr  
485 490 495

Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser  
500 505 510

Thr Ser Ser Gly Gln Gly Gln Asp Leu Pro Pro Glu Lys Thr Tyr  
515 520 525

Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile Gln  
530 535 540

Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr Leu  
545 550 555 560

Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Asp Gly  
565 570 575

Lys Tyr Gln Phe Asp  
580

<210> 14

<211> 3600

<212> DNA

<213> Staphylococcus epidermidis

<220>

<221> CDS

<222> (33)..(3308)

<400> 14

tacattgaaa tagtcaaaga aaaggagttt tt atg att aat aaa aaa aat aat 53  
Met Ile Asn Lys Lys Asn Asn  
1 5

tta cta act aaa aag aaa cct ata gca aat aaa tcc aat aaa tat gca 101  
Leu Leu Thr Lys Lys Pro Ile Ala Asn Lys Ser Asn Lys Tyr Ala  
10 15 20

att aga aaa ttc aca gta ggt aca gcg tct att gta ata ggt gca aca 149  
Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr  
25 30 35

tta ttg ttt ggt tta ggt cat aat gag gcc aaa gcc gag gag aat tca 197  
Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Ser  
40 45 50 55

gta caa gac gtt aaa gat tcg aat acg gat gat gaa tta tca gac agc	245		
Val Gln Asp Val Lys Asp Ser Asn Thr Asp Asp Glu Leu Ser Asp Ser			
60	65	70	
aat gat cag tct agt gat gaa gaa aag aat gat gtg atc aat aat aat	293		
Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn			
75	80	85	
cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa	341		
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu			
90	95	100	
acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag	389		
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu			
105	110	115	
tca aca aca aat gta gat gaa aac gaa gca aca ttt tta caa aag acc	437		
Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr			
120	125	130	135
cct caa gat aat act cat ctt aca gaa gaa gag gta aaa gaa tcc tca	485		
Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser			
140	145	150	
tca gtc gaa tcc tca aat tca tca att gat act gcc caa caa cca tct	533		
Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser			
155	160	165	
cac aca aca ata aat aga gaa gaa tct gtt caa aca agt gat aat gta	581		
His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val			
170	175	180	
gaa gat tca cac gta tca gat ttt gct aac tct aaa ata aaa gag agt	629		
Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser			
185	190	195	
aac act gaa tct ggt aaa gaa gag aat act ata gag caa cct aat aaa	677		
Asn Thr Glu Ser Gly Lys Glu Asn Thr Ile Glu Gln Pro Asn Lys			
200	205	210	215
gta aaa gaa gat tca aca aca agt cag ccg tct ggc tat aca aat ata	725		
Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile			
220	225	230	
gat gaa aaa att tca aat caa gat gag tta tta aat tta cca ata aat	773		
Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn			
235	240	245	

gaa tat gaa aat aag gct aga cca tta tct aca aca tct gcc caa cca	821		
Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro			
250	255	260	
tcg att aaa cgt gta acc gta aat caa tta gcg gcg gaa caa ggt tcg	869		
Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser			
265	270	275	
aat gtt aac cat tta att aaa gtt act gat caa agt att act gaa gga	917		
Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly			
280	285	290	295
tat gat gat agt gaa ggt gtt att aaa gca cat gat gct gaa aac tta	965		
Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu			
300	305	310	
atc tat gat gta act ttt gaa gta gat gat aag gtg aaa tct ggt gat	1013		
Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp			
315	320	325	
acg atg aca gtg gat ata gat aag aat aca gtt cca tca gat tta acc	1061		
Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr			
330	335	340	
gat agc ttt aca ata cca aaa ata aaa gat aat tct gga gaa atc atc	1109		
Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile			
345	350	355	
gct aca ggt act tat gat aac aaa aat aaa caa atc acc tat act ttt	1157		
Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe			
360	365	370	375
aca gat tat gta gat aag tat gaa aat att aaa gca cac ctt aaa tta	1205		
Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu			
380	385	390	
acg tca tac att gat aaa tca aag gtt cca aat aat aat acc aag tta	1253		
Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu			
395	400	405	
gat gta gaa tat aaa acg gcc ctt tca tca gta aat aaa aca att acg	1301		
Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr			
410	415	420	
gtt gaa tat caa aga cct aac gaa aat cgg act gct aac ctt caa agt	1349		
Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser			
425	430	435	

atg ttt aca aat ata gat acg aaa aat cat aca gtt gag caa acg att Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile 440 445 450 455	1397
tat att aac cct ctt cgt tat tca gcc aag gaa aca aat gta aat att Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile 460 465 470	1445
tca ggg aat ggt gat gaa ggt tca aca att ata gac gat agc aca ata Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile 475 480 485	1493
att aaa gtt tat aag gtt gga gat aat caa aat tta cca gat agt aac Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn 490 495 500	1541
aga att tat gat tac agt gaa tat gaa gat gtc aca aat gat tat Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr 505 510 515	1589
gcc caa tta gga aat aat gat gtg aat att aat ttt ggt aat ata Ala Gln Leu Gly Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile 520 525 530 535	1637
gat tca cca tat att att aaa gtt att agt aaa tat gac cct aat aag Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys 540 545 550	1685
gat gat tac acg act ata cag caa act gtg aca atg cag acg act ata Asp Asp Tyr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile 555 560 565	1733
aat gag tat act ggt gag ttt aga aca gca tcc tat gat aat aca att Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile 570 575 580	1781
gct ttc tct aca agt tca ggt caa gga caa ggt gac ttg cct cct gaa Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu 585 590 595	1829
aaa act tat aaa atc gga gat tac gta tgg gaa gat gta gat aaa gat Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp 600 605 610 615	1877
ggt att caa aat aca aat gat aat gaa aaa ccg ctt agt aat gta ttg Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu 620 625 630	1925

gta act ttg acg tat cct gat gga act tca aaa tca gtc aga aca gat			1973
Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp			
635	640	645	
gaa gat ggg aaa tat caa ttt gat gga ttg aaa aac gga ttg act tat			2021
Glu Asp Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr			
650	655	660	
aaa att aca ttc gaa aca cct gaa gga tat acg ccg acg ctt aaa cat			2069
Lys Ile Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His			
665	670	675	
tca gga aca aat cct gca cta gac tca gaa ggt aat tct gta tgg gta			2117
Ser Gly Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val			
680	685	690	695
act att aat gga caa gac gat atg acg att gat agt gga ttt tat caa			2165
Thr Ile Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln			
700	705	710	
aca cct aaa tac agc tta ggg aac tat gta tgg tat gac act aat aaa			2213
Thr Pro Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys			
715	720	725	
gat ggt att caa ggt gat gat gaa aaa gga atc tct gga gtt aaa gtg			2261
Asp Gly Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val			
730	735	740	
acg tta aaa gat gaa aac gga aat atc att agt aca act aca acc gat			2309
Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Asp			
745	750	755	
gaa aat gga aag tat caa ttt gat aat tta aat agt ggt aat tat att			2357
Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile			
760	765	770	775
gtt cat ttt gat aaa cct tca ggt atg act caa aca aca aca gat tct			2405
Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Asp Ser			
780	785	790	
ggt gat gat gac gaa cag gat gct gat ggg gaa gaa gtt cat gta aca			2453
Gly Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr			
795	800	805	
att act gat cat gat gac ttt agt ata gat aac gga tac tat gat gac			2501
Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp			
810	815	820	

gaa tcg gat tcc gat agt gac tca gac agc gac tca gat tcc gat agt			2549
Glu Ser Asp Ser			
825	830	835	
gat tca gac tcc gat agc gac tcg gat tca gac agc gac tca gat tca			2597
Asp Ser			
840	845	850	855
gac agc gac tcg gat tct gat agc gac tcg gat tca gac agc gac tca			2645
Asp Ser			
860	865	870	
gac tca gac agt gat tca gat tca gac agc gac tca gat tcc gat agt			2693
Asp Ser			
875	880	885	
gat tca gac tca gac agc gac tca gat tct gat agt gat tca gac tca			2741
Asp Ser			
890	895	900	
gac agt gat tca gat tca gac agc gac tca gat tcc gat agt gat tca			2789
Asp Ser			
905	910	915	
gac tca gac agc gac tca gat tcc gat agt gat tca gac tca gac agc			2837
Asp Ser			
920	925	930	935
gac tca gat tct gat agt gat tca gac tca gac agt gat tca gac tca			2885
Asp Ser			
940	945	950	
gac agt gat tca gat tcc gat agt gat tca gac tcc gat agc gac tca			2933
Asp Ser			
955	960	965	
gac tcg gat agt gac tca gat tct gat agt gat tca gac tcc gat agc			2981
Asp Ser			
970	975	980	
gac tca gac tcg gat agt gac tca gat tct gat agt gat tca gac tca			3029
Asp Ser			
985	990	995	
gac agc gac tca gat tct gat agt gat tca gac tca gtc agt gat tca			3077
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Val Ser Asp Ser			
1000	1005	1010	1015

gat tcc gat agt gat tca gac tca ggc agt gat tcg gat tcc gat agt 3125  
 Asp Ser Asp Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp Ser Asp Ser  
 1020 1025 1030

gat tca gac tca gac aac gac tca gat tta ggc aat agc tca gat aag 3173  
 Asp Ser Asp Ser Asp Asn Asp Ser Asp Leu Gly Asn Ser Ser Asp Lys  
 1035 1040 1045

agt aca aaa gat aaa tta cct gat aca gga gct aat gaa gat tat ggc 3221  
 Ser Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp Tyr Gly  
 1050 1055 1060

tct aaa ggc acg tta ctt gga act ctg ttt gca ggt tta gga gcg tta 3269  
 Ser Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu  
 1065 1070 1075

tta tta ggg aaa cgt cgc aaa aat aga aaa aat aaa aat taaaatgttc 3318  
 Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn  
 1080 1085 1090

aatgaaatt ttagaaaga agcagatatg agatttgaat agaaagtaga tttagtccaa 3378

caaatgtaag atgttgatta aaactataat ataactttca cgtttatcat atcttgtgaa 3438

aaagatgatg caaacaaggt catttctatt aaaaatgact taaatgtatg attttttagag 3498

aaacatatac aactcacaat ctgacaatga ttaatagag gaaccgtgaa tttaaatga 3558

attcatggtt ctttttatt gaattaataa aaattctttt at 3600

<210> 15  
 <211> 1092  
 <212> PRT  
 <213> *Staphylococcus epidermidis*

<400> 15  
 Met Ile Asn Lys Lys Asn Asn Leu Leu Thr Lys Lys Lys Pro Ile Ala  
 1 5 10 15

Asn Lys Ser Asn Lys Tyr Ala Ile Arg Lys Phe Thr Val Gly Thr Ala  
 20 25 30

Ser Ile Val Ile Gly Ala Thr Leu Leu Phe Gly Leu Gly His Asn Glu  
 35 40 45

Ala Lys Ala Glu Glu Asn Ser Val Gln Asp Val Lys Asp Ser Asn Thr

50	55	60															
Asp	Asp	Glu	Leu	Ser	Asp	Ser	Asn	Asp	Gln	Ser	Ser	Asp	Glu	Glu	Lys		
65					70					75			80				
Asn	Asp	Val	Ile	Asn	Asn	Asn	Gln	Ser	Ile	Asn	Thr	Asp	Asp	Asn	Asn		
								85		90			95			⑥	
Gln	Ile	Ile	Lys	Lys	Glu	Glu	Thr	Asn	Asn	Tyr	Asp	Gly	Ile	Glu	Lys		
								100		105			110				
Arg	Ser	Glu	Asp	Arg	Thr	Glu	Ser	Thr	Thr	Asn	Val	Asp	Glu	Asn	Glu		
								115		120			125				
Ala	Thr	Phe	Leu	Gln	Lys	Thr	Pro	Gln	Asp	Asn	Thr	His	Leu	Thr	Glu		
								130		135			140				
Glu	Glu	Val	Lys	Glu	Ser	Ser	Ser	Val	Glu	Ser	Ser	Asn	Ser	Ser	Ile		
								145		150			155			160	
Asp	Thr	Ala	Gln	Gln	Pro	Ser	His	Thr	Thr	Ile	Asn	Arg	Glu	Glu	Ser		
								165		170			175				
Val	Gln	Thr	Ser	Asp	Asn	Val	Glu	Asp	Ser	His	Val	Ser	Asp	Phe	Ala		
								180		185			190				
Asn	Ser	Lys	Ile	Lys	Glu	Ser	Asn	Thr	Glu	Ser	Gly	Lys	Glu	Glu	Asn		
								195		200			205				
Thr	Ile	Glu	Gln	Pro	Asn	Lys	Val	Lys	Glu	Asp	Ser	Thr	Thr	Ser	Gln		
								210		215			220				
Pro	Ser	Gly	Tyr	Thr	Asn	Ile	Asp	Glu	Lys	Ile	Ser	Asn	Gln	Asp	Glu		
								225		230			235			240	
Leu	Leu	Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	Asn	Lys	Ala	Arg	Pro	Leu		
								245		250			255				
Ser	Thr	Thr	Ser	Ala	Gln	Pro	Ser	Ile	Lys	Arg	Val	Thr	Val	Asn	Gln		
								260		265			270				
Leu	Ala	Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	His	Leu	Ile	Lys	Val	Thr		
								275		280			285				
Asp	Gln	Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	Ser	Glu	Gly	Val	Ile	Lys		
								290		295			300				
Ala	His	Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	Val	Thr	Phe	Glu	Val	Asp		

305	310	315	320
Asp Lys Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn			
325	330	335	
Thr Val Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys			
340	345	350	
Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn			
355	360	365	
Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn			
370	375	380	
Ile Lys Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val			
385	390	395	400
Pro Asn Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser			
405	410	415	
Ser Val Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn			
420	425	430	
Arg Thr Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn			
435	440	445	
His Thr Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala			
450	455	460	
Lys Glu Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr			
465	470	475	480
Ile Ile Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn			
485	490	495	
Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu			
500	505	510	
Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val			
515	520	525	
Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile			
530	535	540	
Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr			
545	550	555	560
Val Thr Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr			

565 570 575  
Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly  
580 585 590  
Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val  
595 600 605  
Trp Glu Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu  
610 615 620  
Lys Pro Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr  
625 630 635 640  
Ser Lys Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly  
645 650 655  
Leu Lys Asn Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly  
660 665 670  
Tyr Thr Pro Thr Leu Lys His Ser Gly Thr Asn Pro Ala Leu Asp Ser  
675 680 685  
Glu Gly Asn Ser Val Trp Val Thr Ile Asn Gly Gln Asp Asp Met Thr  
690 695 700  
Ile Asp Ser Gly Phe Tyr Gln Thr Pro Lys Tyr Ser Leu Gly Asn Tyr  
705 710 715 720  
Val Trp Tyr Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys  
725 730 735  
Gly Ile Ser Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile  
740 745 750  
Ile Ser Thr Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn  
755 760 765  
Leu Asn Ser Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met  
770 775 780  
Thr Gln Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp  
785 790 795 800  
Gly Glu Glu Val His Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile  
805 810 815  
Asp Asn Gly Tyr Tyr Asp Asp Glu Ser Asp Ser Asp Ser Asp Ser Asp

820 825 830  
Ser Asp  
835 840 845  
Ser Asp  
850 855 860  
Ser Asp  
865 870 875 880  
Ser Asp  
885 890 895  
Ser Asp  
900 905 910  
Ser Asp  
915 920 925  
Ser Asp  
930 935 940  
Ser Asp  
945 950 955 960  
Ser Asp  
965 970 975  
Ser Asp  
980 985 990  
Ser Asp  
995 1000 1005  
Ser Asp Ser Val Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Gly  
1010 1015 1020  
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp  
1025 1030 1035 1040  
Leu Gly Asn Ser Ser Asp Lys Ser Thr Lys Asp Lys Leu Pro Asp Thr  
1045 1050 1055  
Gly Ala Asn Glu Asp Tyr Gly Ser Lys Gly Thr Leu Leu Gly Thr Leu  
1060 1065 1070  
Phe Ala Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg

1075

1080

1085

Lys Asn Lys Asn  
1090

1  
Bart